```
OM of: US-09-525-998A-1 to: PIR_68:*  qmt_format : pfs

Date: Apr 23, 2002 10:17 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
 -MODEL=frame+_n2p.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09525998/runat_23042002_132338_10205/app_query.fasta_1 2117
 -DB=PIR_68 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
 -DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
 -ALIGN=15 -MODE=LOCAL  OUTFMT=pfs  NORM=ext -MINLEN=0
 -MAXLEN=2000000000 -USER=US09525998_#COGN1_1_96 -NCPU=6 -TCPU=3
 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-525-998A-1
Query length: 1368
Database: PIR_68:*
Database sequences: 219241
Database length: 76174552
Search time (sec): 113.890000


score_list:
Sequence              Strd Orig    ZScore   EScore Len  ! Documentation  ..
pir1:CQHUT1             + 2487.00 2971.58  2.4e-158  455  ! tumor necrosis factor receptor
pir2:JC4302             + 1738.00 2077.64  2.1e-108  461  ! tumor necrosis factor receptor
pir1:CQRPT1             + 1563.50 1868.69  9.2e-97   461  ! tumor necrosis factor receptor
pir1:GQMST1             + 1521.00 1817.91  6.3e-94   454  ! tumor necrosis factor receptor
pir2:I54182             +  290.00  344.24  8.0e-12  435  ! tumor necrosis factor receptor
pir1:GQHPN              +  240.50  285.10  1.6e-08  427  ! nerve growth factor receptor pr
pir1:A26432             +  223.00  264.18  2.1e-07  425  ! nerve growth factor receptor pr
pir2:B38634             +  205.00  241.84  3.7e-06  474  ! tumor necrosis factor receptor
pir2:I48854             +  204.50  241.47  4.0e-06  459  ! gene murine tumour necrosis fac
pir1:A35356             +  204.00  240.84  4.3e-06  461  ! tumor necrosis factor receptor
pir1:GQVZML             +  200.00  238.56  8.2e-06  326  ! I2 protein - myxoma virus (stra
pir1:JN0006             +  197.50  233.80  1.2e-05  416  ! nerve growth factor receptor, l
pir2:B43692             +  192.00  229.00  2.8e-05  325  ! I2 protein - rabbit fibroma vir
pir2:A46483             +  191.50  228.36  3.0e-05  327  ! apoptosis mediating membrane-as
pir2:JC2395             +  177.00  211.07  0.0003   324  ! Fas antigen precursor - rat
pir2:A40035             +  177.00  210.82  0.0003   335  ! apoptosis-mediating surface ant
pir2:A46476             +  176.50  210.91  0.0003   305  ! B cell-associated surface molec
pir2:F75518             +  175.50  209.37  0.0003   839  ! hypothetical protein - Deinococ
pir2:C13674             +  168.50  196.32  0.0010   999  ! US4 protein - human herpesvirus
pir1:A46517             +  167.00  200.59  0.0013   240  ! CD27 antigen precursor - human
pir2:A60771             +  166.50  199.63  0.0014   277  ! B-cell activation protein CD40
pir2:D72175             +  166.50  197.95  0.0014   349  ! G2R protein - variola minor vir
pir2:T28523             +  164.00  194.98  0.0021   348  ! hypothetical protein G2F - vari
pir2:D36858             +  164.00  194.95  0.0021   349  ! gene G4R protein - variola viru
pir2:A42086             +  159.00  185.11  0.0043   595  ! CD30 antigen precursor - human
pir2:C42125             +  159.00  184.17  0.0042   677  ! trophozoite cysteine-rich surfa
pir2:T14764             +  158.00  190.22  0.0048   999  ! hypothetical protein DKFZp564F0
pir2:I37383             +  157.50  187.94  0.0056   314  ! FAS soluble protein - human
pir1:QQBE1              +  157.00  181.96  0.0057   660  ! BHIF1 protein - human herpesvir
pir2:T09059             +  156.50  173.46  0.0057  1964  ! notch4 - mouse
pir2:S29605             +  156.00  178.63  0.0066   886  ! glycoprotein 350/220 - human he
pir2:A37233             +  155.50  186.03  0.0077   294  ! mucin, tracheal (AMN 22) - huma
pir2:B48423             +  155.50  183.94  0.0075   392  ! homeotic protein engrailed 1 -
pir2:A43942             +  155.50  180.15  0.0065  4020  ! mucin 2 precursor, intestinal
pir2:I22759             +  155.00  179.03  0.0071  2824  ! hypothetical protein F55H12.3
pir2:H84824             +  154.00  180.24  0.0093   518  ! En/Spm-like transposon protein
pir2:T44768             +  152.50  178.18  0.0117   507  ! antifreeze glycopeptide AFGP p
pir2:I48141             +  152.50  177.37  0.0116   591  ! acrogranin - guinea pig (fragme
pir2:B70803             +  152.50  175.85  0.0114   729  ! hypothetical protein R03879.2 -
pir1:QQBE21             +  152.50  174.27  0.0112   987  ! membrane antigen gp350 - human
pir2:A59266             +  152.50  164.42  0.0102  3530  ! unconventional myosin 15 - hum
pir2:I39825             +  151.50  155.59  0.0123  2187  ! nascent polypeptide-associa
pir2:S51939             +  151.00  177.73  0.0149   439  ! chitinase (EC 3.2.1.14) prec
pir2:F86387             +  151.00  173.76  0.0143   760  ! probable pto kinase interact
pir2:A61183             +  150.50  179.61  0.0164   312  ! hypothetical protein (sdsB r

seq_name: pir1:CQHUT1

seq_documentation_block:
tumor necrosis factor receptor 1 precursor [validated] - human
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C;Accession: A38208, A34899, A34900, A36555, G36555, A38281, S12057, JT0758, A60231;
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to
A;Reference number: A38208; MUID:92250049
A;Accession: A38208
A;Molecule type: DNA
A;Residues: 1-455 <FUC>
A;Cross-references: GB:M75964; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A;Reference number: A34899; MUID:90235284
A;Accession: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <LOE>
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A;Experimental source: placenta
A;Note: part of this sequence, including the amino end of the mature protein, confirm
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A;Reference number: A34900; MUID:90235285
A;Accession: A34900
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:M32315; NID:g339741; PIDN:AAA36753.1; PID:g339745
R;Himmler, A.; Master Peggy, I.; Kroenke, M.; Schoutens, T.; Fiers-Walter, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A;Reference number: A36555; MUID:91090841
A;Accession: A36555
A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: G36555
A;Molecule type: protein
A;Residues: 23-38;47-53;'X';55-79;'XX';82-94;'XX';97-104;107-128;162-167;'X';16
A;Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A;Reference number: A38281; MUID:91017209
A;Accession: A38281
A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtm
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF Rs). The cDNA for the
le form of the receptor.
A;Reference number: S12057; MUID:91116021
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <NOP>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: parts of soluble TNF binding protein 1 (sTBP-1), its amino- and carboxyl ends
R;Kemper, O.; Wallach, D.
Gene 134, 269-276, 1993
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A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758; MUID:94085779
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2 terminal amino acid sequenc
A;Reference number: A60231; MUID:90292116
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A;Reference number: A38258; MUID:91062364
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
A;Reference number: A60594; MUID:89171156
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XA',60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, T.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2265-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A;Reference number: JC2404; MUID:95128033
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
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C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
Quality: 2487.00 Length: 455
Ratio: 5.466 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x GQHUT1 ..

Align seq 1/1 to: GQHUT1 from: 1 to: 455

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     67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 84

    251 GTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117

    351 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 400
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134

    401 ATATATGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
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    134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150

    451 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 500
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    201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217

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    217 lIlePhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetT 234

    701 ATCGCTACCAACGGTGGAAGTCCAAGCTTACTCCATTGTTTGTGGGAAA 750
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    234 yrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGlyLys 250

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    251 SerThrProGluLysGluGlyGluLeuGluGlyThrThrThrLysProLe 267

    801 GGCCCAAATCTAAGCTTCAGTCCTATTCCAGCTTTCATCCCCATCCTGG 850
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    267 uAlaProAsnProSerPheSerProThrProGlyPheThrProIleLeuG 284

    851 GCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900
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     301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317

     951 CTATCAGGGGGCTGACCCCATCCTTGCGACAGCCTCGCCTCCGACGCCA 1000
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     317 oTyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProI 334

    1001 TCCCCAACCCCCTTCACAACTGGCAGGACAGGGCCCACAAGCCACAGACC 1050
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     334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350

    1051 CTACACACTGATGACCCCGCCACGCTGTACGCCGTGGTGCACAACGTGCC 1100
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     351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr 367

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    1151 AGATCGATCGGCTGGAGCTGCAGAACGGCCGCTGCCTGCGCGAGGCGCAA 1200
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     384 luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

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     401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417

    1251 GCTGGAGCTGTTGGGAGTGGTTGTTCCGGACTTGAAGTCTGGTTGGT 1300
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     417 rLeuGluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL 434

    1301 TGGAGGACATCGAGGAGGCGCTTTGCGGCCCCCCCCCCCTCCCCGCCC 1350
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seq_name: pir2:JC4302

seq_documentation_block:
tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302, PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48439.1; PID:g1141753
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
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C;Keywords: glycoprotein, kidney, receptor, transmembrane protein, tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
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F;84-126/Domain: NGF receptor repeat homology <NGF>
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F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
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              Ratio:  4.526                 Gaps:      4
 Percent Similarity:  83.117   Percent Identity: 71.645%

alignment_block:
 US-09-525-998A-1 x JC4302  ..

 Align seq 1/1  to: JC4302  from: 1  to: 461

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      34 roGlyAspArgGluLysArgLeuSerLeuCysProGlnGlyTyrSer 50

     151 CACCCtCAAAAtAAttGCAttCCtGtAtCAAGtGtCACAAAGGAACCtA 200
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     201 CttGtACAAtCAtCtGtCCACGCCCCGCCtACGAtATGGACtCCAGGCAGt 250
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      84 ysAspAsnGlyThrPheThrAlaSerGluAsnHisLeuThrGlnCysLeu 100

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     101 SerCysSerLysCysArgSerGluMetSerGlnValGlnIleSerProCy 117

     351 CACAGtGGACGGGGACAGCGtGtGtGGGtGCAGGAAGAACCAGtACGGC 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgL 134

     401 AttAttGGAGtGAAAACCttttCCAGtGCttCAAttGCAGCCtCtGCCtC 450
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     134 ysTyrTrpSerGluThrLeuPheGlnCysLeuAsnCysSerLeuCysPro 150

     451 AATGGGACCGtGCACCtCtGCtGCCAGGAGAAACAGAACACCGtGtGCAC 500
         ||||||:|:|:::::||   |||   |:|||||||:::|||||:::::
     151 AsnGlyThrValGlnLeuProCysLeuGluLysGlnAspThrIleCysAs 167

     501 CTGCCATGCAGCtCtCttCtCtAACAGAAAACGAGtGtGtCtCCtGtAGtA 550
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     167 nCysHisSerGlyPhePheLeuArgAspLysGluCysValSerCysValA 184

     551 ACtGtAACAAAAGCtTGGAGtGCACGAAGttGtGGCtACCCCAGAttGAC 600
         |||||||:::::   :::|||   :::|||||||                |||
     184 snCysLysAsnArg   AspCysLysAspLeuCysProAlaThrSerGlu 199

     601 AAtGttAAGGGCACtGAGGACtCAGGCACtACAGtGCtGttGCCCtGGt 650
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     200 ThrArgAsnAspPheGlnAspThrGlyThrThrValLeuLeuProLeuVa 216

     651 CAttttt:::CCt:ttGCCttttAtCC:CCtCttCAtCCttAAtGt 700
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     216 lIlePheThrLeuGlyLeuCysLeuAlaPheLeuLeuValLeuAlaC 233

     701 AtCCtAttAAGtttGAAGtCCAAGttAtAtttAttGttGtGGGAAA 750
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     233 ysArgTyrLeuAsnSerProSerLysAspValTyrIleProAlaSerAsp 249

     751 tcGACACtttAAAAAGAGCCGGAGTTtGAAGGAAtACtACtAAGCtC.. 798
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     266 rPheGlyProIleThrThrPheSerPro'ePro'erPheSerProThrT 283

     848 TGGGCTTCACTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCCTAT 897
     283 hrThrPheSerProValProSerPheSerProIleSerSerProThrPne 299

     898 ACCCCCGCTGACTGTCCCAACTTT      GCCCCTCCCCGCAGAGAGGT 941
     300 ThrProCysAspTrpSerAsn'leLysValThrSerProProLysGluIl 316

     942 GGCACCACCCTATCAGGGGGCTGACCCCATCCTTGCGACAGCCCTCGCCT 991
     316 eAlaProProProGlnGlyAlaGlyProIleLeuProMetProProAlaS 333

     992 CCGACCCCATCCCCAACCCCTTCAGAAGTGGCAGGACAGCGCCCACAAG 1041
     333 erThrProValProThrProLeuProLysTrpGlyGlySerAlaHisSer 349

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     350 AlaHisSerAlaProAlaGlnLeuAlaAspAlaAspProAlaThrLeuTy 366

    1080 CGCCGTGGTGGAGAACGTGCCCCCGTTGCCTGGAAGGAATTCGTGTGGC 1129
     366 rAlaValValAspGlyValProProThrArgTrpLysGluPheValArgA 383

    1130 GCCTAGGGCTGAGCGACCACGACATCGATCGGCTGGAGCTGCAGAACGGG 1179
     383 rqLeuGlyLeuSerGluHisGluIleGluArqLeuGluLeuGlnAsnGly 399

    1180 CGCTGCCTGCGCGAGGCCAATACACCATGCTGCCCACCTGCAGGCCCCC 1229
     400 ArqCysLeuArgGluAlaGlnTyrSerMetLeuAlaGluTrpArgArgAr 416

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     416 qThrSerArgArgGluAlaThrLeuGluLeuLeuGlySerValLeuArgA 433

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     433 spMetAspLeuLeuGlyCysLeuGluAspIleGluAlaLeuArqGly 449

    1330 CCCGCCGCCCTCCGCCCGCCCACTCTTCTCAGA 1365
     450 ProAlaArgLeuAlaProAlaProHisLeuLeuArg 461

seq_name: pir1:GQRTT1

seq_documentation_block:
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Mauror-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted


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alignment_block:
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      51 GCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACC 100
      17 aLeuLeuMetGlyIleHisProSerGlyValThrGlyLeuValProSerL 34

     101 TAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATC 150
      34 euGlyAspArgGluLysArgAspAsnLeuCysProGlnGlyLysTyrAla 50

     151 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
      51 HisProLysAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

     201 CTTGTACAATGACTGTCCAGGCCCGGGGCAGCATACGGACTGCAGGCAGT 250
      67 rLeuValSerAspCysProSerProGlyGlnGluThrValCysGluValC 84

     251 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
      84 ysAspLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeu 100

     301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGTGGAGATCTCTTCTTG 350
     101 SerCysLysThrCysArgLysGluMetPheGlnValGluIleSerProCy 117

     351 CACAGTGCACCGGCACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 400
     117 sLysAlaAspMetAspThrValCysGlyCysLysLysAsnGlnPheGlnA 134

     401 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
     134 rgTyrLeuSerGluThrHisPheGlnCysValAspCysSerProCysPhe 150

     451 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 500
     151 AsnGlyThrValThrIleProCysLysGluLysGlnAsnThrValCysAs 167

     501 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGACTCTCTCCTGTAGTA 550
     167 nCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrProCysSerH 184

     551 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600
     184 isCysLysLysAsnGlnGluCysMetLysLeuCysLeuProProValAla 200

     601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGT 650
     201 AsnValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuVa 217

     651 CATTCTCTTGGCTCTTGCCTTTACGCCTCTTCATTGGTTTAATCT 700
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     |||||||:::|||||||||||||||||   ::::::   |||:::|||:::
   217 IlePheLeuGlyLeuCysLeuLeuPhePheIleCysIleSerLeuLeuC 234

   701 AlGGCIACCAACGGTGGAAGTCTAAGTCTACTCCATTGTTGTGGGAAA 750
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   234 ysArgTyrProGlnTrpArgProArgValTyrSerIleIleCysArgAsp 250

   751 TCGACACCTGAAAAAGAGGGGCAGCTTCAAGGAACTACTACTAAGCCCCT 800
       |||:::|||   ||||||   |||   ||||||   :::|||||||||||
   251 SerAlaProValLysGluValGluGlyGlyGlyIleValThrLysProLy 267

   801 GGCCCCAAAC     CCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCA 844
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   267 ulhrProAlaSerIleProAlaPheSerProAsnProGlyPheAsnProI 284

   845 CCCTGGGCTTCAGTCCTGTGCCCAGTTCCACCTTCACCTCCAGCTCCACC 894
       ||||||||||||||   :::|||      :::          |||||||||
   284 hrLeuGlyPheSerThrThrProArgPheSerHisProValSerSerThr 300

   895 ..............IAIACCCCCGGTGACTGTCCCAACTTTGCGGCTCC 929
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   301 ProIleSerProValPheGlyProSerAsnTrpHisAsnPheValProPr 317

   930 CCGCAGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCTTGCGA 979
       |   ||||||||||:::|||      |||||||||||||:::|||
   317 oValArgGluValValProThr...GlnGlyAlaAspProLeuLeuTyrC 333

   980 CAGCCCTCGCCTCGGATCCCATCCCCAACCCCTTCAGAAGTGGGAGGAC 1029
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   350 ValValAlaAlaGlnProGlnArgLeuAspThrAlaAspProAlaMetLe 366

  1077 GTACGCCGTGGTGGAGAACCTCCCCCCGTTCCCCTGGAAGGAATTCGTGC 1126
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   366 ulyrAlaValValAspGlyValProProThrArgTrpLysGluPheMetA 383

  1127 GGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAAC 1176
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   383 rgLeuLeuGlyLeuSerGluHisGluIleGluArgLeuGluLeuGlnAsn 399

  1177 GGGCGCTGCCTGCGCGAGCGCCAATACACCATGCTGCGACGTGCAGGCC 1226
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   400 GlyArgCysLeuArgGluAlaHisTyrSerMetLeuGluAlaTrpArgAr 416

  1227 GCGCAGCGCCGCGCCCAGGGCAGCCGCATGCAGCTGCTGCCAGCGCTGCC 1276
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   416 gArgThrProArgHisGlnAlaThrLeuAspValValGlyArgValLeuC 433

  1277 GCGACATGGACGTGCTCGGCTCGCTGGACGACATCGACGAGGTGCTTTGC 1326
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   433 ysAspMetAspLeuArgGlyCysLeuGluAspIleArgGluThrLeuGlu 449

  1327 CGCCCCGCC 1335
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   450 SerProAla 452

seq_name: pir1:GQMST1

seq_documentation_block:
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; I54532; I57826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A:Reference number: A38634; MUID:91187885
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g340768; PIDN:AAA40770.1; PID:g340769
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO2>
A:Cross-references: GB:M59465; NID:g339825; PIDN:AAA40771.1; PID:g339826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kiesselbachis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAK>
A:Cross-references: EMBL:X59796; NID:g54848; PIDN:CAA41922.1; PID:g54849
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Int receptor type b.
A:Reference number: S19021; MUID:92039815
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A:Reference number: I54532; MUID:94245292
A:Accession: I54532
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g440733
R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis fact
A:Reference number: I57826; MUID:93156721
A:Accession: I57826
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-393,'G',395-454 <RP2>
A:Cross-references: GB:M76454; NID:g202101; PIDN:AAA40455.1; PID:g202102
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha
C:Genetics:
A:Gene: TNFR-2
A:Introns: [illegible]
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane pro
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F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-212/Domain: extracellular #status predicted <EXT>
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F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
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F:236-454/Domain: intracellular #status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted


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 Percent Similarity:  87.596   Percent Identity:  83.188

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seq_name: pir2:I54182

seq_documentation_block:
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May 1996 #sequence_revision 24 May 1996 #text_change 17 Mar 2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a human cDNA library of human 12p transcribed seq
A;Reference number: I54182; MUID:93252381
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

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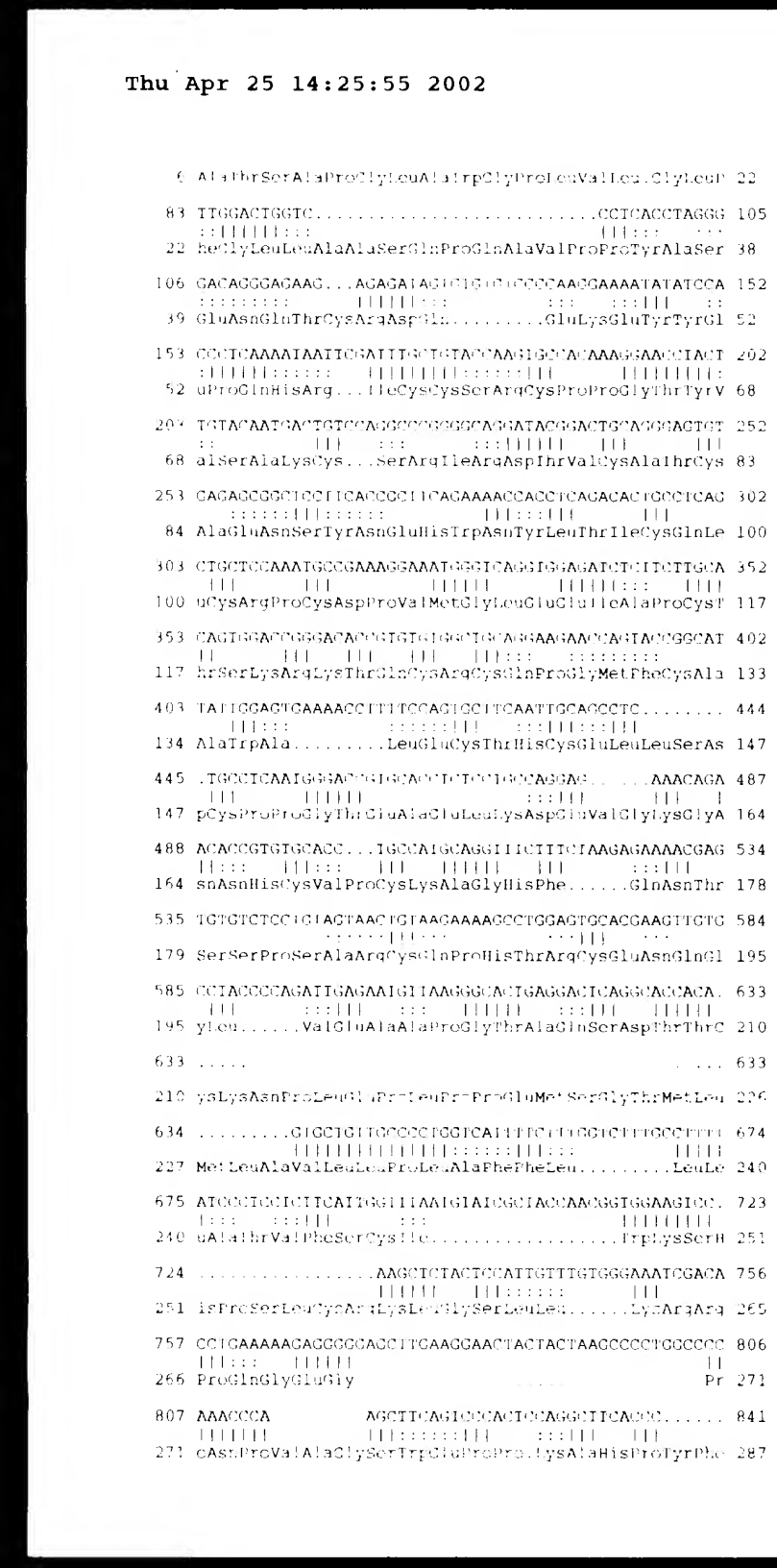

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seq_documentation_block:
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C;Species: Homo sapiens (man)
C;Date: 31 Mar-1988 #sequence_revision 31 Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218, A60274, B21689, I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor
A;Reference number: A25218; MUID:87051745
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:g184; PIDN:AAA51544.1; PID:g189205
R;Marano, N.; Dhotre, B.; Eadie, J.G.; Schattman, G.; Thompson, S.; Grob, J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth fa
A;Reference number: A60204; MUID:87085574
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'I',33-42,'TI',45-46,'IX',50-51,'XX',54-56,<MAR>
A;Experimental source: melanoma cell line AM75

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A;Note: this sequence has been corrected by a note added in proof to follow the nucleoti
R;Vissavajjhala, P., Leszyk, J.D., Lin Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor, NGF receptor repeat homology
C;Keywords: duplication, glycoprotein, heterodimer, monomer, phosphoprotein, receptor, t
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F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TPM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted


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              Ratio:  1.108                 Gaps:     25
 Percent Similarity:  44.569   Percent Identity: 23.819

alignment_block:
 US-09-525-998A-1 x GQHUN  ..

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      13 ProArgLeuLeuLeuLeuLeuLeuGlyValSerLeuGlyGlyAla.. 28

      84 TGGACTGGTCCCTCACCTAGGGACAGGGAGAAGAGAGATAGTGTGTGTC 133
                                                 :::::::||||
      29 .....lysGluAlaCysP 33

     134 CCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAG 183
         ||   |||   |||   |||          ::::::   ||||||
      33 roThrGlyLeuTyrThrHis ...  ...SerGlyGluCysCysLysAla 46

     184 TGCCACAAAGGAACCTACTTGTACAATGACTGCCCACGCCCCGGGCAGGA 233
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      47 CysAsnLeuGlyGluGlyValAlaGlnProCys...GlyAlaAsnGln.. 61

     234 TACGGACTGCAGGGAGTGT   GAGAGGGCTCCTTCACCGCTTCAGAAA 280
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      62 .ThrValCysGluProCysLeuAspSerValThrPheSerAspValValS 78

     281 ACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGT 330
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      92 LeuGlnSerMetSerAlaProCysValGluAlaAspAspAlaValCysAr 108

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     108 gCys    .... AlaTyrGlyTyrTyrGlnAspGlnTrpThrGlyArgC 122

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     122 ysGluAlaCysArgValCysGluAlaGlySerGlyLeuValPheSerCys 138

     475 CAGGACAAACAGAACACCGTGTGC...ACCTGCCATGCAGGTTTCTTCT 521
         |||:::|||||||||||||||||      |||      |||   :::
     139 GlnAspLysGlnAsnThrValCysGluGluCysProAspGlyThrTyrSe 155

     522 AAGAGAA            AACGAGTGTGTCTCCTGTAGTAACTGT      555
             |||            :::   |||:::   |||:::   |||
     156 rAspGluAlaAsnHisValAspProCysLeuProCysThrValCysGluA 172

     556         AAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATT 597
                 ::::::      ||||||||||:::   :::      :::
     172 spThrGluArgGluLeuArgGluCysThrArgTrpAlaAspAlaGluCys 188

     598 GAGAATGTTAAGGGCACTGAGGACACAGGCACCACAGTGCTGTTGCCCCT 647
         |||.....  |||
     189 GluGluIleProGly..................................... 193

     648 GGTCATTTTCTTTGGTCTTTGCCTTTTATGCCTCCTCTTCATTGGTTTAA 697

     193 ..................................................... 193

     698 TGTATGCCTACCAACGGTGGAAGTCCAAGCTCTACTGCATTGTTTGTGGG 747
                    ||||||                    :::
     194 ...  .     ArgTrp                .     IleThrArg 198

     748 AAATCGACACCTGAAAAACAGGGGGAGCTTGAAGCAACTACTACTAAGCC 797
         ::::::  ||||||  :::  :::        ::|||  :::||
     199 SerThrProProGluGlySerAspSerThrAlaProSerThrGlnGluPr 215

     798 CCTGGCCCCAAACCCAAGC          TTCAGTCCCACTCCAGGCTTCA 838
         |   ||||||   :::          |||  :::  |||   :
     215 GGluAlaProProGlyGlnAspLeuIleAlaSerThrValAlaGlyValV 232

     839 CCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGC 888
         ::  |||:::     |||     |||     |||     ::::::
     232 alThrThrValMetGlySerSerGlnProValValThrArgGlyThrThr 248

     889 TCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCT            927
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     249 AspAsnLeuIleProValTyrCysSerIleLeuAlaAlaValValValG 265

     928 .....CCCCGCAGAGAGGTGGCACCACCCT 952
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     265 yLeuValAlaTyrIleAlaPheLysArgTrpAsnSerCysLysGlnAsnL 282

     953 ATCAGGGGGCTGAC      CCCATCCTTGCGACAGCCCTCGCCTCCGAC 996
          ||||||||||:::      |||:::     |||
     282 ysGlnGlyAlaAsnSerArgProValAsnGlnThr.............. 293

     997 CCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGC       GCCCACAA 1040
         |||   |||:::      :::      :::|||||||      :::
     294 ProProProGluGlyGluLysLeuHisSerAspSerGlyIleSerValAs 310

    1041 GCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCC....... 1083
          |||||||||      ::::::|||   |||      |||
     310 pSerGlnSerLeuHisAspGlnGlnProHisThrGlnThrAlaSerGlyG 327

    1084 .....GTGGTGGAGAACGTGCCCCCGTTGCGC 1110
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     327 lnAlaLeuLysGlyAspGlyGlyLeuTyrSerSerLeuProProAlaLys 343
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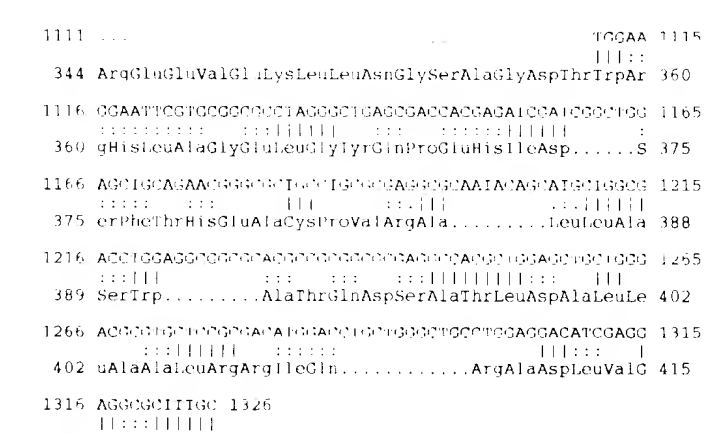

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seq_name: pir1:A26431

seq_documentation_block:
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M. J.; Misko, T. P.; Hsu, C.; Herzenberg, L. A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Metsis, M.; Timmusk, T.; Arumäe, U.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor, NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-149/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted


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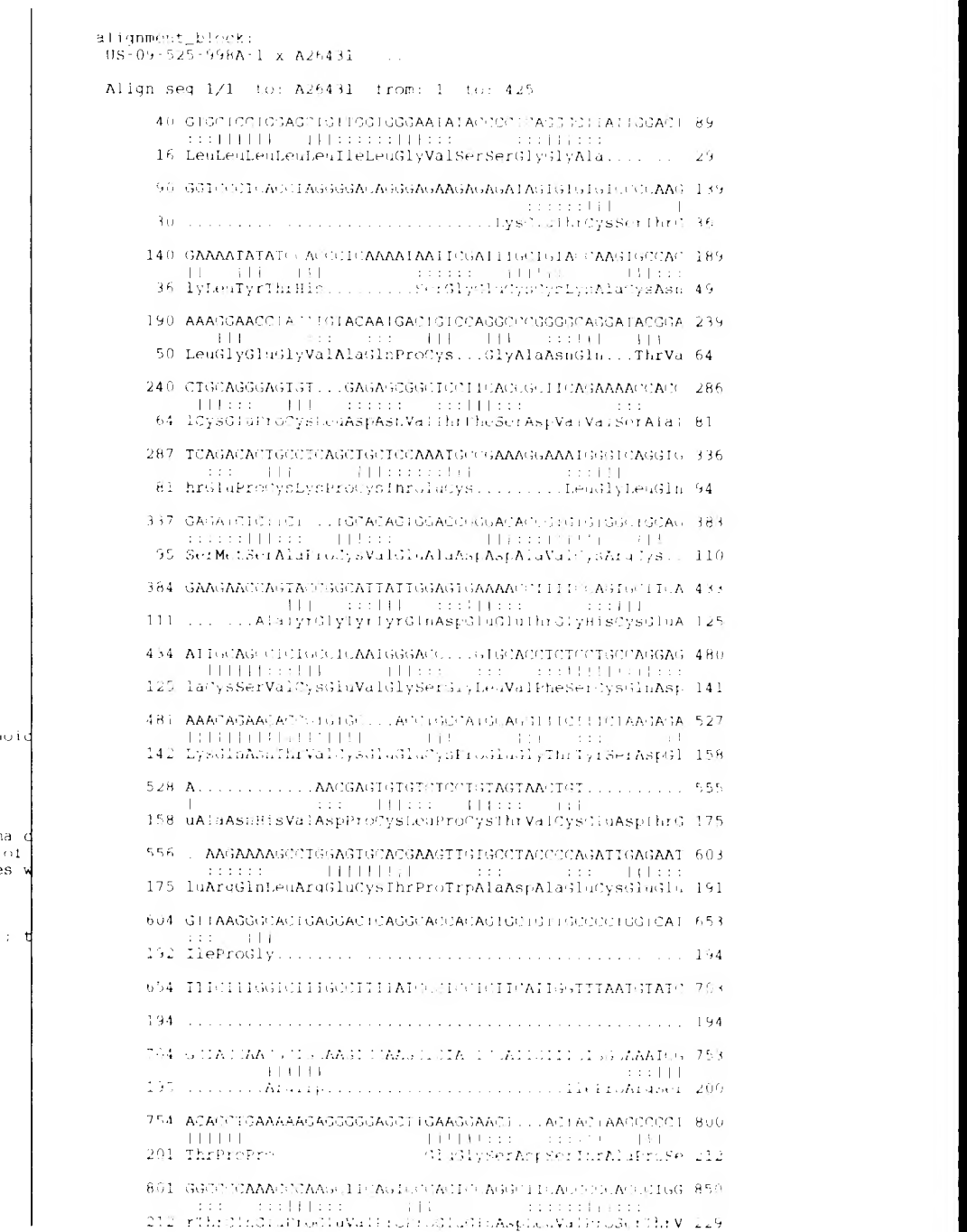

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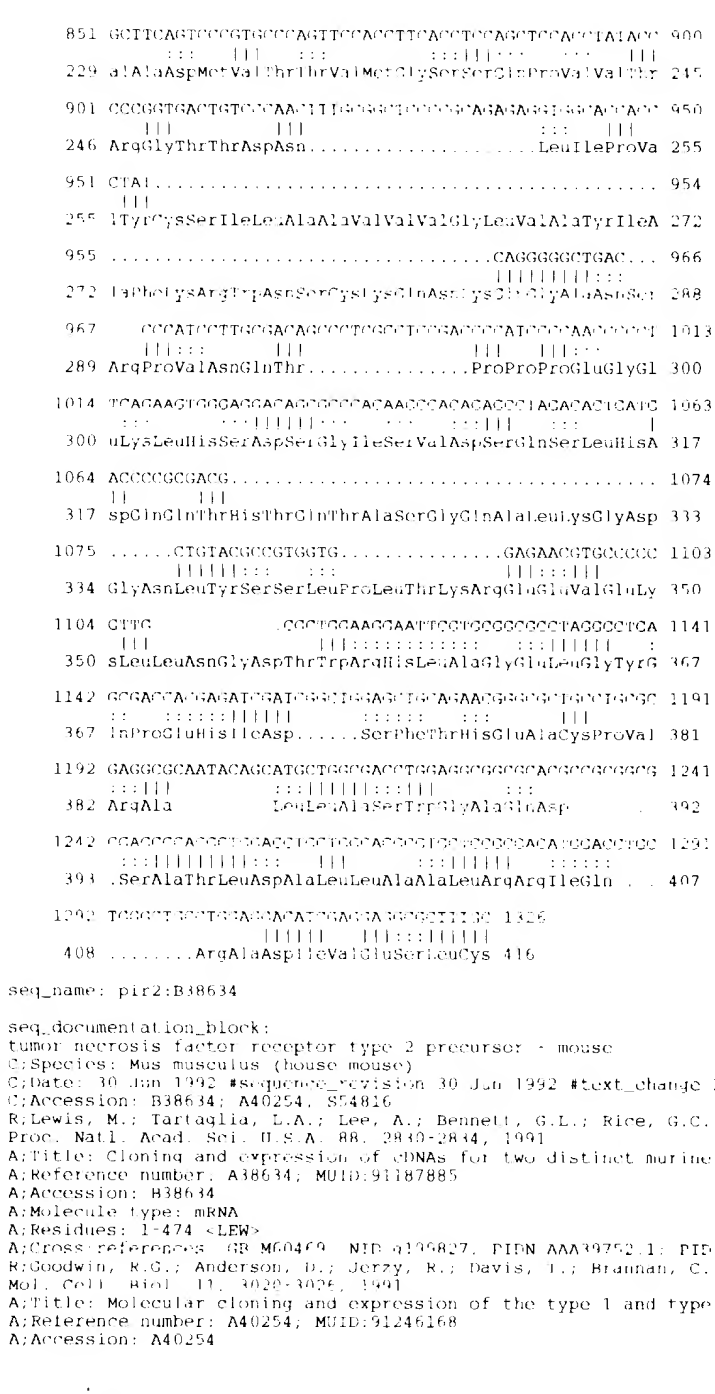

seq_name: pir2:B38634

seq_documentation_block:
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254, S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A;Reference number: A38634; MUID:91187885
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75 TNF receptor
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

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US-09-525-998A-1 x B38634 ..

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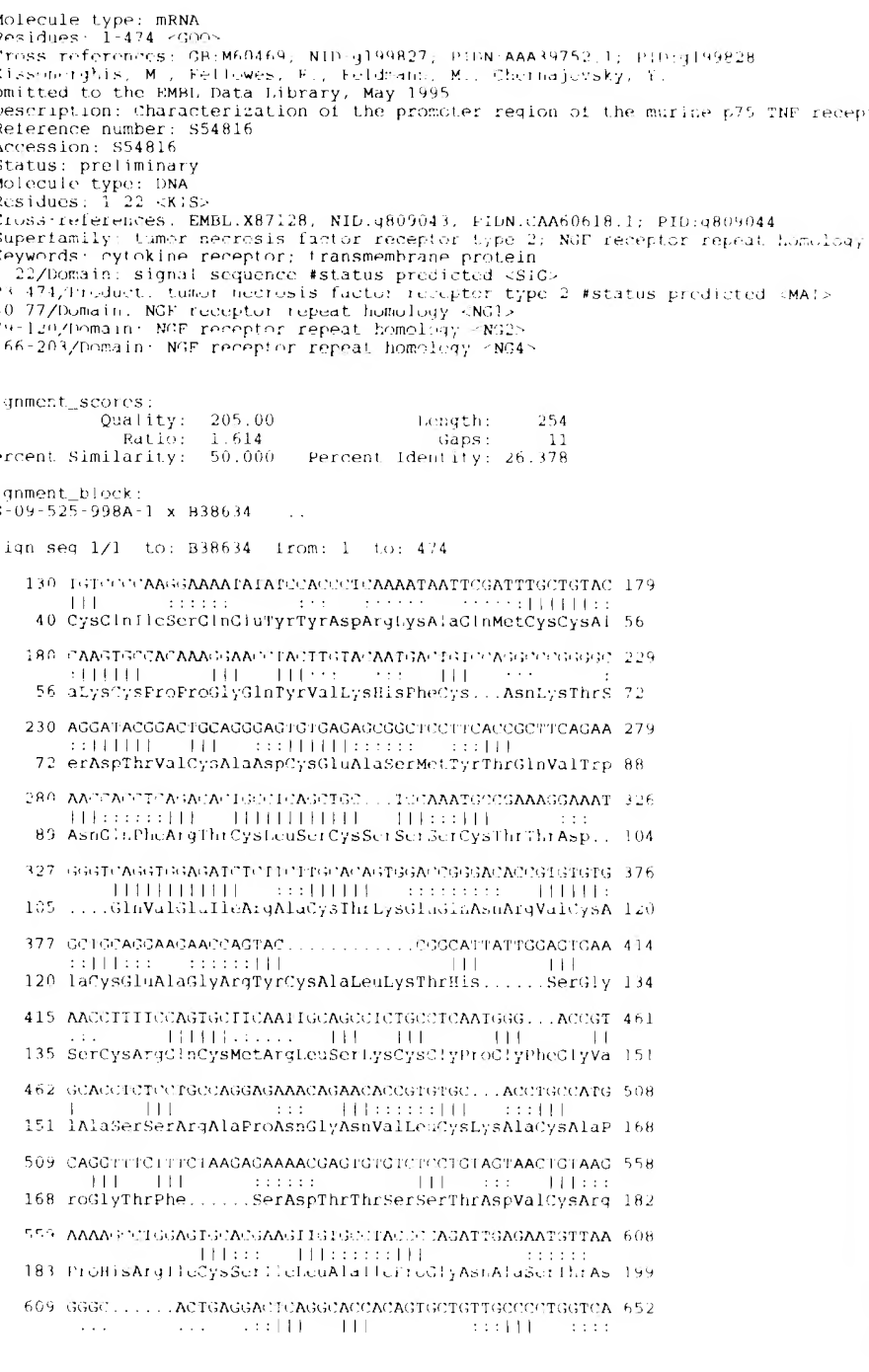

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     199 pAlaValCysAlaProGluSerProThrLeuSerAlaIleProArgThrL 216

     653 TTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTAT 702
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     216 euTyrVal..................................... 218

     703 CGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATC 752
                                                        ||
     219 .....................................................Se 219

     753 GACACCTGAAAAACAGCCCCAGCTTGAAGCAACTACTACTAAGCCCCTCG 802
         |   ||||||                        |||   :::::||||||
     219 rGlnProGlnPro.................ThrArgSerGlnProLeuA 230

     803 CCCCAAAGCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGC 852
             :::||:::   |||   ||||||:::::     :::||||||
     230 spGlnGluProGlyProSerGlnThrProSerIleLeuThrSerLeuGly 246

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seq_name: pir2:I48854

seq_documentation_block:
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23 Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848
A;Accession: I48854
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2, NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>


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alignment_block:
 US-09-525-998A-1 x I48854   ..

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     180 CAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGC 229
         :||||||       |||   |||:::   :::   |||   ...   :
      41 alysCysProProGlyGlnTyrValLysHisPheCys...AsnLysThrS 57

     230 AGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAA 279
         ::|||||||   |||   :::|||||||::::::   :::|||
      57 erAspThrValCysAlaAspCysGluAlaSerMetTyrThrGlnValTrp 73

     280 AACCACCTCAGACACTGCCTCAGCTGC...TCCAAATGCCGAAAGGAAAT 326
         |||::::::|||   ||||||||||||   |||:::|||      :::
      74 AsnGlnPheArgThrCysLeuSerCysSerSerSerCysSerThrAsp.. 89

     327 GGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTG 376
             |||||||||      :::||||||   :::::::::   ||||||:
      90     GlnValGluThrArgAlaCysThrLysGlnGlnAsnArgValCysA 105

     377 GCTGCAGGAAGAACCAGTAC.............CGGCATTATTGGAGTGAA 414
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         ::|||:::   :::::::|||                |||       |||
     105 laCysGluAlaGlyArgTyrCysAlaLeuLysThrHis.....SerGly 119

     415 AACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGG...ACCGT 461
         :::      |||||||:::::   |||   |||       |||      ||
     120 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVa 136

     462 GCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGC...ACCTGCCATG 508
         |       |.|          :::   ||||:::::|||   :::||
     136 lAlaSerSerArgAlaProAsnGlyAsnValLeuCysLysAlaCysAla 154

     509 CAGGTTTCTTTCCAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAG 558
           |||   |||      ::::::          |||   :::   ||||::
     153 roGlyThrPhe. ....SerAspThrThrSerSerThrAspValCysArg 167

     559 AAAAGCCTGGACTGCACGAAGTTGTGCCTACCC..... ... 593
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     168 ProHisArgIleCysSerIleLeuAlaIleProGlyAsnAlaSerThrAs 184

     593 ..... .. .... .. ..... . . ..... 593

     184 pAlaValCysAlaProGluSerProThrLeuSerAlaIleProArgThrI 201

     594 ..... ....CAGATTGAGAATGTT 606
                              :::::::::
     201 euTyrValSerGlnProGluProThrArgSerGlnProLeuAspGlnGlu 217

     607 AAGGGCAGTGAGGACTCA.....CCCAGCACA.. 633
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     218 ProGlyProSerGlnThrProSerIleLeuThrSerLeuGlySerThrPr 234

     634 .....GTGCTGTTGCC TGGTCATTT 655
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     234 olleIleGlnGlnSerThrLysGlyGlyIleSerLeuProIleGlyLeuI 251

     656 TCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGC 705
         ::   |||:::      ||||:::|||||||:::::|||||||:
     251 leValGlyValThrSerLeuGlyLeuLeuMetLeuGlyLeuVal..... 265

     706 TACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGAC 755
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     266 ..................AsnCysPheIleLeuValGluArgLysLysLy 276

     756 ACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCC 805
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     276 sProSerCys.........LeuGluArgAspAlaCysValThrAsnVal 290

     806 CAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTC 855
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     290 roAspGluLysSerGlnAspAlaValGlyLeuGluGlnGluHisLeuLeu 306

     856 AGTCCCGTGCCCAGTTCCACCTTCACCTCC...AGCTCCACCTATACCCC 902
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     307 ThrThrAlaProSerSerSerSerSerSerLeuGluSerSerAlaSerAl 323

     903 CGGTGAC......TGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCAC 946
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     323 aGlyAspArgArgAlaProProGlyGlyHisProGlnAlaArgValMetA 340

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     340 laGluAlaGlnGlySerGlnGluAlaArgAlaSerSerArgIleSerAsp 356

seq_name: pir1:A35356

seq_documentation_block:
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor, TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec 2000
C;Accession: A35356, A38475, A49475, A49482, A23667, B45916, I36694
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
Science 248, 1019-1023, 1990
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A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.J.; Schwartz, D.R.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
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A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
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C;Keywords: duplication; glycoprotein; receptor, transmembrane protein
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F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
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F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

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174 CTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 223
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 53 sCysSerLysCysSerProGlyGlnHisAlaLysValPheCysThr...L 69

224 CGGGCCAGGATACCGACTGCAGGGAGTGTGACACCGGCTCCTTCACCCCT 273
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 69 ysThrSerAspThrValCysAspSerCysGluAspSerThrTyrThrGln 85

274 TCAGAAACCACTTCAGACACTGCCTCAGCTGC...TCCAAATGCCGAAA 320
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 86 LeuTrpAsnTrpValProGluCysLeuSerCysGlySerArgCysSerSe 102

321 GGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCG 370
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102 rAsp      GlnValGluThrGlnAlaCysThrArgGluGlnAsnArgI 117

371 TGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
    ::|||   ||||||   :::              |||          |||
117 leCysThrCysArgProGly..............TrpTyrCysAlaLeu 128

421 TICCAGIGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 470
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129 SerLysGlnCluGlyCysArgLeuCysAla..................... 148

471 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC 520
                          :::      ||:::   ||||||   :
139 ...................ProLeuArgLysCysArgProGlyPheGlyV 149

521 TA....         AGAGAAAACGAGTGTGTCTCCTGTAGTAACTGT... 555
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149 alAlaArgProGlyThrGluThrSerAspValValCysLysProCysAla 165

556             AAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCC.. 591
                .........  :::   |||   :::|||   |||
166 ProGlyThrPheSerAsnThrThrSerSerThrAspIleCysArgProHi 182

592 TAGATTGAGAATGTTAAGGGCACTGAGGACTTAGGCACTACTAGTTTT 640
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182 sGlnIleCysAsnVal.........................ValAlaI 190

641 TGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATT 690
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190 lePro..................................................... 191

691 GGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGT 740
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192 .........................GlyAsnAlaSerMetAspAlaVa 199

741 TTGTGGGAAATCGACTCTGAAAAAGAGGGGGACTTGAAGGAACTACTA 790
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199 lCysThrSerThrSerPro ..............................T 206

791 CTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840
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      ||:::  :::|||||||:::            |||  |||     |||
    206 hrArgSerMetAlaProGlyAlaValHisLeuProGlaProValSerThr 222

    841 CCCACCCTGGGCTTCAGTCCCGTGCCCAGT...TCCACCTTCACCTCCAG 887
        :::          :::|||:::|||:::   ||||||      |||::
    223 ArgSerGlnHisThrGlnProThrProGluProSerThrAlaProSerTh 239

    888 CTCCACCTATACCCCC.....................GGTGACTGTC 913
        :|||         ||!                    ||||::
    239 rSerPheLeuLeuProMetGlyProSerProProAlaGluGlySerThrG 256

    914 CCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCIATCAGGGGGCT 963
        :::||||||  |||          ::::::                |||
    256 lyAspPheAlaLeuProValGlyLeuIleValGly......ValThrAla 270

    964 GACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCT 1013
            :::|||     ::::::::::::     |||  :::   ::
    271 LeuGlyLeuLeuIleIleGlyValValAsnCysValIleMetThrGlnVa 287

   1014 TCAGAAGTGGGAGGACAAGCCCCACAAGCCACAGAGCCTAGACACTGATG 1062
        :::|||                  ||||||     |||:::  :::
    287 IlysLys..... .....LysProLeuCysLeuGlnArgGluA 298

   1063 A..............CCCCGCGACGCTGTACGCCGTGGTGGAGAACGT 1097
                       |||  |||  :::|||      |||  :::
    298 laLysValProHisLeuProAlaAspLysAlaArg......GlyThrGln 312

   1098 GCCCCCGTTGCGCTGGAAGCAATTCGTGCGGCGCCTAGGGCTGAGCGACC 1147
        :::|||      :::  :::  :::|||||||  ::::::
    313 GlyProGluGlnGlnHisLeuLeuIleThrAlaProSerSerSerSerSe 329

   1148 ACGA...GATGGATCTGGCTGGAGCTGCAGAACGGGGGCTGCCTGCGCGAG 1194
            :::  |||||||:::|||  :::|||     |||:::|||:
    329 rSerLeuGluSerSerAlaSerAlaLeuAspArgArgAlaProThrArgA 346

   1195 GCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGA 1244
        ::      |||      |||  :::|||||
    346 snGlnProGlnAlaProGly   ValGluAla...  .      .. 355

   1245 GGCCACCGTGCAGCTGCTGCCAGGCGTGCTCCGCCACATGGACCTCTGG 1294
             :::|||||||:::  :::||||||        :::     ::
    356 .....SerGlyAlaGlyGluAlaArgAlaSerThrGlySerSerAspSe 370

   1295 GCTGCCTGGAGGACAT 1310
        :  ||||||||||||
    370 rSerProGlyGlyHis 375

seq_name: pir1:GQVZML

seq_documentation_block:
12 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M87976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein, NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted


alignment_scores:
            Quality:  200.00              Length:     240
              Ratio:  1.695                 Gaps:      10
 Percent Similarity:  49.162   Percent Identity:  25.833
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alignment_block:
 US-09-525-998A-1 x GQVZML  ..

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      40 GTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACT 89
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       6 LeuLeuLeuAlaTyrValAlaCysValTyrGlyGlyGly........... 18

      90 GGTCCCTCACCTACGCGACAGGGACAAGACAGACATACTGTGTGTCCCCAAA 139
         :::|||:::   :::||||||   :||          |||      :
      19 .AlaProTyrGlyAlaAspArgGlyLys.............CysArgGlyA 31

     140 GAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACCAAGTGCCAC 189
         ::   |||          ::::::::::::::::|||||||||:::|||
      31 snAspTyr.........GluLysAspGlyLeuCysCysThrSerCysPro 44

     190 AAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGA 239
         ||||:::||      :::   |||   ||||:::|:::||||||
      45 ProGlySerTyrAlaSerArgLeuCys...GlyProGlySerAspThrVa 60

     240 CTGCAGCGAGTGTGAGAGCGGCTCCTTCACCGCTCAGAAAACACCTCA 289
         |||      |||::::::   ::::|||||||||||   ||||||
      60 lCysSerProCysLysAsnGluThrPheThrAlaSerThrAsnHisAlaI 77

     290 GACACTGCCTCAGCTGC...TCCAAATGCCGAAAGCAAATGGCTCAGGTG 336
         || :::|||||   :::::::|      :::::::::
      77 roAlaCysValSerCysArgLysGlyArgCysThrGlyHisLeuSer..... 91

     337 GAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGCTGCAGGAA 386
         |||   :::|| ||      ||||||   |||||   |||
      92 GluSerGlnSerCysAspLysThrArgAspArgValCysAspCysSerAl 108

     387 GAACCAGTAC.. ..... 396
         ::::::|||
     108 aGlyAsnTyrCysLeuLeuLysGlyGlnGluGlyCysArgIleCysAlaP 125

     396 ..... 396

     125 roLysThrLysCysProAlaGlyTyrGlyValSerGlyHisThrArgThr 141

     397 .........................CGGCATTATTGGAGTGAAAACCT 419
                                  ||::::   :::|||:::   ::
     142 GlyAspValLeuCysThrLysCysProArgTyrThrTyrSerAspAlaVa 158

     420 TTTCCAGTGCTTCAATTGCAGCCCTCTGCCTCAATGGC...ACCGTGCACC 466
         :  :::     :::|||:::     ::::::      :::|||:::::
     158 lSerSerThrGluThrCysThrSerSerPheAsnTyrIleSerValGluP 175

     467 TCTCCTGCCAGGAGAAACACAACACCGTGTGCACCTGTCATCAGGTTTC 516
         :::::              ::::::|||   ||||||      ||||||
     176 hcAsnGluTyrProValAsnAspThrSerCysThrThrThrAlaGly... 190

     517 TTTCTAAGAGAAAACGAGTGTGTCCCTGTAGTAACTGTAAGAAAAGCCT 566
                 |||||   |:::::   |:::::   :::   :::|
     191 .... ....ProAsnGluValValLysThrSerGlyThrSerValThrIle 204

     567 C.........GAGTCCACGAAGGTTGTGCCTACCCCAGATTCAGAATGTTA 607
         |         :::||    :::      :::      :::::::
     204 GAsnHisThrAspCysAspProValPheHisThrGlyTyrTyrGlyThrS 221

     608 AGGGCACTGAGGACTCAGCC 627
         ::|||::::||   ::::||
     222 erGlyGlnGlyAsnGlyAsp 227

seq_name: pir1:GN0006

seq_documentation_block:
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 15-Sep-1989 #sequence_revision 15-Sep-1989 #text_change 10-Sep-1999
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C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in t
A;Reference number: JN0006; MUID:90166579
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140
A;Accession: A60504
A;Status: preliminary, not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Superfamily: nerve growth factor receptor, NGF receptor repeat homology
C;Keywords: duplication, glycoprotein, heterodimer, monomer, phosphoprotein, receptor; t
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted


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alignment_block:
 US-09-525-998A-1 x JN0006   ..

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       31 CTGCCACTGGTGCTCCTGCAGCTGTTGGTGGGAATATACCCCTCAGGGCT 80
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        5 ValProLeuLeuLeuLeu..............LeuLeuProAlaGly.. 15

       81 TATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGT 130
                     !!!      !!!::::::::!!!!!!             !
       16 .............ProThrTrpGlySerLysGluLys............C 24

      131 GTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||           !!!            :::::::::   !!!!!!
       24 ysLeuThrLysMetTyr.........ThrThrSerGlyGluCysCysLys 37

      181 AAGTCCCACAAAGGAACCTACTTCTACAATCACTGTCCAGGCCCGGGGCA 230
             !!!::   !!!      :::   :::   !!!   !!!   :::!!
       38 AlaCysAsnLeuGlyGluGlyValValGlnProCys...GlyValAsnGl 53

      231 GGATACGGACTGCAGGAGTGT...GAGAGCGGCTCCTTCACCGCTTCAG 277
          |   !!!   !!!:::   !!!   ...!!!   :::::::::::::::
       53 n...ThrValCysGluProCysLeuAspSerValThrTyrSerAspThrV 69

      278 AAAACCACCTCAGACACTGCCTCACCTGCTCCAAATGCCGAAAGGAAATG 327
          :::      :::   !!!      !!!::::::!!!         :::
       69 alSerAlaThrGluProCysLysProCysThrGlnCys.........Val 82

      328 GGTCAGCTGGAGATCTCTTCT...TGCACAGTGGACCGGGACACCGTGTG 374
          !!!      :::::::!!:::   !!!:::   :::   !!!:::!!!!!
       83 GlyLeuHisSerMetSerAlaProCysValGluSerAspAspAlaValCy 99

      375 TGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCC 424
          |   !!!           !!!   ......   ::!!!          :
       99 sArgCys.........AlaTyrGlyTyrPheGlnAspGluLeuSerGlyS 113

      425 AGTGCTTCAATTGCAGCCTCTGCCTCAATGGG...ACCGTGCACCTCTCC 471
          ::!!!   :::!!!!!!.::!!!      !!!      :::   :::
      113 erCysLysGluCysSerIleCysGluValGlyPheGlyLeuMetPhePro 129

      472 TGCCAGGAGAAACAGAACACCGTGTGC   ACCTGCCATGCAGGTTTCTT 518
          !!!::::::::::!!!:::!!!!!!!!      !!!      !!!   !!
      130 CysArgAspSerGlnAspThrValCysGluGluCysProGluGlyThrPh 146

      519 TCTAAGAGAA............AACGAGTGTGTCTCCTGTAGTAACTGTA 556
          |     !!!           :::   !!!:::   !!!:::   !!!:
      146 eSerAspGluAlaAsnPheValAspProCysLeuProCysThrIleCysG 163

      557 AGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAGAATGTT 606
          ::::::::          :::!!!   !!!
      163 luGluAsnGluValMetValLysGluCys..................... 172

      607 AAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTT 656
             :::!!!::::!!:::            !!!   !!!
      173 ThrAlaThrSerAspAlaGluCysArgAspLeuHisPro............ 185

      657 CTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCI 706

      185                                                    185

      707 ACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACA 756
             !!!!!!   ...   !!!      ...!!!. ::::::
      186 .....ArgTrpThrThrHisThrProSerLeu...AlaGlySerAspSer 199

      757 CCTGAAAAAGAGGGGCAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCC 806
          !!!!!!                                !!!::::::::
      200 ProGlu.......                          ProIleThrAr 205

      807 AAACCCAAGCTTCAGTCCACTCCAGGCTTCACCCCCACCCTGGGCTTCA 856
          ...!!!   !!!...   !!!   !!!.:::::   !!!!!! !!!:::
      205 gAspPro   PheAsn   ThrGluGlyMetAlaThrThrLeu.AlaAsp 219

      857 GTCCCGTGC.....................CCAGTTCCACCTTCACCTCC 885
          :::                          !!!!!!
      220 IleValThrThrValMetGlySerSerGlnProValValSerArgGlyTh 236

      886 AGCTCCACCTATACCCCCGGTGACTGTCCCAACTTGCGG  ....... 925
           !!!      :::   !!!!!!          !!!
      236 rAlaAspAsnLeuIleProValTyrCysSerIleLeuAlaAlaValValV 253

      926 ..... .....CTGCCCGCAGAGAGGTGGCAGCACCCTATCAGG 958
                   :::      :::!!!!!!!::      :::
      253 alGlyLeuValAlaTyrIleAlaPheLysArgTrpAsnSerCysLysGln 269

      959 GGGCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAAC 1008
          :::          :::   :::::!!!         !!!!!!!!!!!!
      270 AsnLysGlnGlyAlaAsnAsnArgProValAsnGlnThrProSerProGl 286

     1009 CCCCTTCAGA            ACTGGGAG           ...GACAGCG 1033
               :::              !!!!!!                :::!!!
      286 uGlyGluLysLeuHisSerAspSerGlyIleSerValAspSerGlnSerL 303

     1034 CCCAC      AAGCCACAGAGCCTAGACACTGATGACCCCGCG..... 1071
             !!!      :::!!!   :::   :::!!:::   !!!!!!
      303 euHisAspGlnGlnProProAsnGlnSerThrGlnGlyProAlaProLys 319

     1072 ........ ACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGC.. 1110
                  :::!!!!!!!!!!          .:::::!!!!!!   :::
      320 GlyAspGlySerLeuTyrAla.........SerLeuProProSerLysGl 333

     1111          .. .. .. .. .                    .TGGAAGG 1117
                                                    !!!:::
      333 nGluGluValGluLysLeuLeuSerSerSerAlaGluGluThrTrpArgG 350

     1118 AATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGACCGATGGCGTGGAG 1167
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      350 InLeuAlaGlyGluLeuGlyTyrLysGluAspLeuIleAsp..... 363

     1168 CTGCAGAACGGGCGCTGCCTGCGCGAGGGCAA          TACAGCAT 1208
                                                      ....:
      364 ..............CysPheThrArgGluGluSerProAlaArgAla 375

     1209 GCTGCGCACCTGGACGGCGCCCACGCCGCGGCGCAGGCCACGCTGCAGC 1258
          :|||||   |||          :::   ::::::   ||||||||||:::
      375 aLeuAlaAspTrp.....SerAlaLysGluThrAlaThrLeuAspA 389

     1259 TGCTGGCACGCGTGCTCCCCACATGCACCTCCTCGCCTCCTGCAGCAC 1308
            |||      :::|||||||   ::::::                 |||
      389 laLeuLeuValAlaLeuArgLysIleGln.....ArgGlyAsp 401

     1309 ATCGAGGAGCCGCTT 1324
          |||   |||:::|||
      402 IleAlaGluSerLeu 406

seq_name: pir2:B43692

seq_documentation_block:
T2 protein   rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A;Reference number: A43692; MUID:87321103
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein, NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>


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alignment_block:
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        1 MetLeuArgLeuIleAlaLeuLeuValCysValValTyrValTyrGlyAs 17

       75 AGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGAGATA 124
          :               |||||:::   :::::::::   |||
       17 pAsp.....ValProTyrSerSerAsnGluGlyLys..... 27

      125 GTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGC 174
                |||          |||          ::::::::::::::|||
       28 .....CysGlyGlyHisAspTyr.....GluLysAspGlyLeuCys 39

      175 TGTAGCAAGTGCCACAAAGGAACCTATTGTACAATCACTGTGCAGGCCC 224
          |||::::::|||||   |||   |||      :::   |||   |||||
       40 CysAlaSerCysHisProGlyPheTyrAlaSerArgLeuCys   GlyPr 55

      225 CGGCCAGGATACGGATTCGACTCCACTCTGCACGCCGCTGCTTCACCGCT 274
          |||:::::::|||   |||      |||||||::|||:::|||||||||
       55 oGlySerAsnThrValCysSerProCysGluAspGlyThrPheThrAlaS 72

      275 CAGAAAACCACCTCACACACTGCCTCAGCTGC...TCCAAATGCCGAAAG 321
          ||   ||||||         |||:::|||||   :::   |||
       72 erThrAsnHisAlaProAlaCysValSerCysArgGlyProCysThrGly 88

      322 CAAATCCCTCAGGTGCACATCTCTCTTCTCACACTCCACTTTCCACACCCT 371
          :::::::::       |||   :::   |||       :::|::   ||
       89 HisLeuSer.....GluSerGluProCysAspArgThrHisAspArgVa 103

      372 CTGTCCCTCCAGCAACAACCACTACCCCAATTATTCCACTTAAAACTTTT 421
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      104 lCysAsnCysSerThrGlyAsnTyrCysAsnLeuGlyGlnAsn..... 118

      422 TCCAGTGCTTCAATTGCAGCCTGTGCCTCAATGGGACCGTGCACCTCTCC 471
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      119 .....GlyCysArgIleCysAlaProGlnThr..... 127

      472 TGCCAGGAGAAACAGAACACCGTGTGCACCTGCCACAGCTTTCTTTCT 521
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      128 ......................  ...LysCysProAlaGlyTyrGlyVa 145

      522 AAGACAAAACCACTGTGTGTCTCTGTACTAACTTAAGAAAAGCCTGGAGT 571
          :      :::       ::::::   :::   ||||:::|||
      146 lSerGlyHisThrArgAlaGlyAspThrLeuCysThrLys..... 148

      572 GCACGAAGTTGTGCCTACCCCAGATT......GAGAATGTTAAGGGCACT 615
                  |||   |||:::          :::::::::::   |||
      149 .....CysProProHisThrTyrSerAspSerLeuSerProThr 161

      616 CAGGACTCAGGACACCACAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCT 665
          |||      |||||||::
      162 GluArgCysGlyThrSer..................................... 167

      666 TTGCCTTTTACTCCTCCTCTTCATTGCTTTAATGTATGCCTACCAACGGT 715
                                                :::::::::
      168 .....................................PheAsnTyrIleSerV 173

      716 GGAAGTGCAAATTGTACTCCATTGTTTGTGGGAAATGGATACTCTAAAAA 765
                ::|||||||   :::
      173 alGlyTheAsnLeuTyrProVal............................ 180

      766 CAGCCCACCTTGAAGGAACTACTACTAAGCCCCTGCCCCCAAACCCAAG 815
          ::::||   :::   ||||||:|          ||,   :::   ::
      181 ...AsnGluThrSerCysThrThrThr.....AlaGlyHisAsnGl 193

      816 CTTCAGTCCTACTCCAGGCTTCACCCCCACCCTGGGCTTCAGT.. .... 858
          :          |||      ||||||   ||||||||||||||
      194 uValIleLysThrLysGluProThrValThrCysAsnTyrThrAspCysA 210

      859 ..CCCGTGCCAGTTCCACCTCCAGCTCC 891
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      210 spProValPheHisThrGluTyrTyrAlaThrSer 221

seq_name: pir2:A46484

seq_documentation_block:
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1993 #sequence_revision 19-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkl
J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A;Reference number: A46484; MUID:92148151
A;Accession: A46484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <WAT>
A;Cross-references: EMBL:M83649; NID:g191225; PIDN:AAA37911.1; PID:g193226
A;Experimental source: BAM3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable elem
A;Reference number: A47254; MUID:93184776
A;Accession: A47254
A;Status: preliminary
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A;Molecule type: nucleic acid
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A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>


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alignment_block:
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       7 ValLeuProLeuValLeuAlaGlySerGlnLeuArgValHisThrGlnGl 23

      78 GGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAG         .A 118
         |:::   ::::::         |||      |||::::::
      23 yThrAsnSerIleSerGluSerLeuLysLeuArgArgArgValHisGluT 40

     119 GAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCG 168
         ||::::  |||  ::|||  |||          |||::::::
      40 hrAspLysAsnCysSerGluGlyLeuTyr.....GlnGlyGlyPro 58

     169 ATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCC 218
         :::||||||     ||::::  |||           :::|||||||
      54 PheCysCysGlnProCysGlnProGlyLysLysValGluAspCysGly 70

     219 AGGCCCGGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGCTCCTTCA 268
             |||          |||      |||   ::::|||:::
      70 sMetAsnGlyGlyThrProThrCysAlaProCysThrGluGlyLysGlaT 87

     269 CGGTTCAAAAAGTACTGTAGA...CACTGCCTCAGCTGCTCCAAATGC 315
         :::::::|||||           |||      |||:::   |||
      87 yrMetAspLysAsnHisTyrAlaAspLysArgCysArgArgCysThrLeuCys 103

     316 CGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTGCACACTGGACCCGGA 365
         ::|||   |||            ::::::||||||::   :::::
     104 AspGluGluHisGlyLeuGluValGluThrAsnCysThrLeuThrGlnAs 120

     366 CACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAA 415
         :|||   |||  |||:::   :::  |||            |||  :
     120 nThrLysCysLysCysLysProAspPheTyrCysAsp.....SerProG 135

     416 ACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCAC 465
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     566 TGGAGTGCAGGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACT 615
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     165 erProArgAsnArgLeuTrpLeu........................... 172

     616 GAGCACTCAGCCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCT 665
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     173 ............LeuThrIleLeu.......................Va 177

     666 TTGCCTTTTATCCCCTCCTCTTCATTGGTTTAATGTATGGCTACCAACGG. 714
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     715 ..TGGAACTGCAAGCTCTACTGCATTGTTTGTGCCAAATCCACACCTCAA 762
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     763 AAACAGCCCGCAGCTTGAACGAACTACTACTAAGCCCCTGGCCCCAAACCC 812
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     204 .SerArgThrSerSerArgGlu............................ 210

     813 AAGCTTCAGTCCCACTCCAGGCTTCA 838
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     211 .....ThrIleProMetAsnAlaSer 217

seq_name: pir2:JC2395

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20 Feb 1995 #sequence_revision 20 Feb 1995 #text_change 05 Nov 1999
C;Accession: JC2395, PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat l
A;Reference number: JC2395; MUID:94128114
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A;Introns: 62/1
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C;Keywords: transmembrane protein
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F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>


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alignment_block:
 US-09-525-998A-1 x JC2395   ..

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      23 yThrAspSerIlePheGluGlyLeuGluLeuLysArgSerValArgGlu. 39

     116 AGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAAT 165
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      40   ThrAspAsnAsnCysSerGluGlyLeuTyr          GlnValGly 52

     166 TCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTG 215
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513 TTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGT......A 556
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137 ..............AspHisCysTyrHisCysThrSerCysCysLeuG 148

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654 TTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATC 703
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176 eLeuProGly.....LeuAlaIleLeuPheValPheIleTyrLysA 190

704 GCTACCAACGGTGGA.........................AGTCC 723
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